

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Baker, Joffre
 Chien, Kenneth
 King, Kathleen
 Pennica, Diane
 Wood, William
- 10 (ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
 Therefor
- 15 (iii) NUMBER OF SEQUENCES: 8
- 20 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 460 Point San Bruno Blvd
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94080
- 25 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: patin (Genentech)
- 30 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE: 05-AUG-1994
 (C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 08/233609
 (B) FILING DATE: 25-APR-1994
- 40 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Hasak, Janet E.
 (B) REGISTRATION NUMBER: 28,616
 (C) REFERENCE/DOCKET NUMBER: 894P1
- 45 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 415/225-1896
 (B) TELEFAX: 415/952-9881
 (C) TELEX: 910/371-7168
- 50 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1352 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900
 5 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950
 GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000
 10 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050
 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100
 15 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA 1150
 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC 1200
 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA 1250
 25 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300
 AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350
 30
 AA 1352

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTATTCGGA CCCC GGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50
 50 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100
 GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA 150

CACATTGGGA ATGAAACAGA GTACCTCCAC TGTAAAAAG AGGGAAGTCA 1100
AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150
TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200
AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250
CTCTCTTTCC GTCTTTTGT AGAAATTCT CAAAATAAAC TCTTATTAA 1300
TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTGAA AATACTTTTT 1350
TT 1352

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Gln	Arg	Glu	Gly	Ser	Leu	Glu	Asp	His	Gln	Thr	Asp	Ser	1	5	10	15
Ser	Ile	Ser	Phe	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr	20	25	30	
His	Asn	Leu	Ala	Arg	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu	35	40	45	
Glu	Glu	Tyr	Val	Gln	Gln	Gln	Gly	Glu	Pro	Phe	Gly	Leu	Pro	Gly	50	55	60	
Phe	Ser	Pro	Pro	Arg	Leu	Pro	Leu	Ala	Gly	Leu	Ser	Gly	Pro	Ala	65	70	75	
Pro	Ser	His	Ala	Gly	Leu	Pro	Val	Ser	Glu	Arg	Leu	Arg	Gln	Asp	80	85	90	
Ala	Ala	Ala	Leu	Ser	Val	Leu	Pro	Ala	Leu	Leu	Asp	Ala	Val	Arg	95	100	105	
Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg	110	115	120	

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Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala
125 130 135

Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Ala Arg Gly Pro
140 145 150

Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser
155 160 165

Thr Ala Gly Ile Phe Ser Ala Lys Val Leu Gly Phe His Val Cys
170 175 180

Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly
185 190 195

Gln Leu Val Pro Gly Gly Val Ala
200 203

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp
1 5 10 15

Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp
20 25 30

Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn
35 40 45

Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser
50 55 60

Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu
65 70 75

Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu
80 85 90

Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe
95 100 105

His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala
110 115 120

Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro
125 130 135

Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
140 145 150

Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
155 160 165

Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
170 175 180

Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
185 190 195

Asn Asn Lys Lys Met
200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50

AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100

GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150

ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200

GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250

CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300

5 ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350

CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA 400

10 GGACGCGGCG CGCCAGGCCCG GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450

TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCCGCC 500

15
GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550

GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550

20 GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600

GCGACCTGGG CCAGCTGCTG CCCGGGGGGCT CGGCCTGAGC GCCGCGGGGGC 650

25 AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700

AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700

30 GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750

ATTGCCTCGG CCTTCTTTGC TTTTGTGGG GGAGAGGGGA GGGGACGGGC 800

35 AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850

AGGGTCTCTG TCGCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACATGC 850

AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900

40 AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA 950

AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTATTATAA 950

45 TTTTGTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAAC 1000

CCGGGGGCTCA AGCGATCC 1018

50

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1018 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50
10 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100
CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150
15 TGC GACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200
CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250
GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300
25 TGC GCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350
GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400
CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450
35 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500
CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCACGA 550
40 CCCCAGGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600
CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650
45 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700
CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750
TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCC 800

TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG 850

TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG 900

TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950

AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 1000

GGCCCCGAGT TCGCTAGG 1018

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ser	Arg	Arg	Glu	Gly	Ser	Leu	Glu	Asp	Pro	Gln	Thr	Asp	Ser
1				5				10						15

Ser	Val	Ser	Leu	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr
			20					25						30

His	Ser	Leu	Ala	His	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu
			35					40						45

Gln	Glu	Tyr	Val	Gln	Leu	Gln	Gly	Asp	Pro	Phe	Gly	Leu	Pro	Ser
			50					55						60

Phe	Ser	Pro	Pro	Arg	Leu	Pro	Val	Ala	Gly	Leu	Ser	Ala	Pro	Ala
			65					70						75

Pro	Ser	His	Ala	Gly	Leu	Pro	Val	His	Glu	Arg	Leu	Arg	Leu	Asp
			80					85						90

Ala	Ala	Ala	Leu	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Asp	Ala	Val	Cys
			95					100						105

Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg
			110					115						120

Arg	Leu	Glu	Asp	Ala	Ala	Arg	Gln	Ala	Arg	Ala	Leu	Gly	Ala	Ala
			125					130						135

Val	Glu	Ala	Leu	Leu	Ala	Ala	Leu	Gly	Ala	Ala	Asn	Arg	Gly	Pro
			140					145						150

	Arg	Ala	Glu	Pro	Pro	Ala	Ala	Thr	Ala	Ser	Ala	Ala	Ser	Ala	Thr
					155					160					165
5	Gly	Val	Phe	Pro	Ala	Lys	Val	Leu	Gly	Leu	Arg	Val	Cys	Gly	Leu
					170					175					180
	Tyr	Arg	Glu	Trp	Leu	Ser	Arg	Thr	Glu	Gly	Asp	Leu	Gly	Gln	Leu
					185					190					195
10	Leu	Pro	Gly	Gly	Ser	Ala									
					200	201									